

Unit	Score	Query	Length	DB	ID	Description
1	989.8	99.7	1401	4	US-09-585-876-1	Sequence 1, Appl1
2	145.2	14.6	1578	3	US-09-044-4094-1	Sequence 1, Appl1
3	145.2	14.6	1578	4	US-09-586-924-1	Sequence 1, Appl1
4	99.4	10.0	1020	4	US-09-170-4960-31	Sequence 31, Appl1
5	99.4	10.0	1900	4	US-09-016-434-1484	Sequence 1484, Appl1
6	99.4	10.0	1901	4	US-08-153-848-43	Sequence 43, Appl1
7	99.4	10.0	1901	3	US-09-299-8434-43	Sequence 43, Appl1
8	99.4	10.0	1901	3	US-09-088-3378-43	Sequence 43, Appl1
9	99.4	10.0	1901	5	PCT-US93-11153-43	Sequence 43, Appl1
10	99.4	10.0	2453	5	PCT-US95-07189-1	Sequence 1, Appl1
11	96.2	9.7	1020	4	US-09-170-4960-181	Sequence 181, Appl1
12	92	9.3	1255	1	US-08-097-938-3	Sequence 3, Appl1
13	92	9.3	1255	1	US-08-476-000-3	Sequence 3, Appl1
14	92	9.3	1255	1	US-08-472-840-3	Sequence 3, Appl1
15	92	9.3	1255	2	US-08-476-976-3	Sequence 3, Appl1
16	92	9.3	1255	3	US-08-474-410-3	Sequence 3, Appl1
17	92	9.3	1255	3	US-08-486-673B-3	Sequence 3, Appl1
18	90	9.1	1224	2	US-08-742-440A-1	Sequence 1, Appl1
19	90	9.1	1414	1	US-08-476-000-62	Sequence 62, Appl1
20	90	9.1	1414	1	US-08-472-840-62	Sequence 62, Appl1
21	90	9.1	1414	1	US-08-476-976-62	Sequence 62, Appl1
22	90	9.1	1414	2	US-08-474-410-62	Sequence 62, Appl1
23	90	9.1	1414	3	US-08-486-673B-62	Sequence 62, Appl1
24	85.6	8.6	1567	3	US-08-489-108-16	Sequence 16, Appl1
25	85.6	8.6	1567	5	PCT-US94-10356-16	Sequence 16, Appl1
26	85.6	8.6	2706	2	US-08-454-549-1	Sequence 1, Appl1
27	85.6	8.6	2706	3	US-08-454-552-17	Sequence 1, Appl1

28	85.2	8.6	1452	1	US-08-149-033A-3	Sequence 3, Appl1
29	85.2	8.6	1452	1	US-08-911-245-3	Sequence 3, Appl1
30	85.2	8.6	1452	1	US-08-553-056C-3	Sequence 3, Appl1
31	85.2	8.6	1452	2	US-08-514-451A-3	Sequence 3, Appl1
32	85.2	8.6	1452	3	US-09-170-371-3	Sequence 3, Appl1
33	85.2	8.6	1452	3	US-09-510-471-3	Sequence 3, Appl1
34	85.2	8.6	1452	3	US-09-048-916B-3	Sequence 3, Appl1
35	84.4	8.5	1551	4	US-09-016-434-139	Sequence 1233, Ap
36	84.4	8.5	1551	4	US-09-023-655-1186	Sequence 1186, Ap
37	84.4	8.5	1780	4	US-09-054-272-1	Sequence 1, Appl1
38	83.2	8.4	1098	4	US-09-170-496D-225	Sequence 225, Appl
39	82.4	8.3	2706	3	US-08-676-351-1	Sequence 1, Appl1
40	81.6	8.2	1098	4	US-09-170-496D-117	Sequence 117, Appl
41	81.6	8.2	1597	2	US-08-724-974A-1	Sequence 1, Appl1
42	81.6	8.2	1697	2	US-09-364-425B-86	Sequence 26, Appl
43	81.4	8.2	1164	4	US-09-170-496D-107	Sequence 107, Appl
44	81.4	8.2	1164	4	US-09-170-496D-221	Sequence 221, Appl
45	81.4	8.2	2051	4	US-09-016-434-1359	Sequence 1233, Ap

ALIGNMENTS

Query Match	Best Local Similarity	Score	DB #	Length
99.7%	99.8%	989.8	4	1401
Matches	991	Conservative	0	Mismatches
			2	Indels
			0	Gaps

D	b	545	TCCTTGTATGTCAACATGTACAGAGTATTTATTTCTGACCGTGTAGTGTGTGGCT	604
Q	y	361	TTCTGCGCAATGTTCAACCCCTTTGGCTTCTGATGTCAACCAGATCAGAGTCCTTGG	420
D	b	605	TTCTGCGCAATGTTCAACCCCTTTGGCTTCTGATGTCAACCAGATCAGAGTCCTTGG	664
Q	y	421	ATCTCTGTGGGATTCATATGATCTCTTATCAGTGGCTCTCTCAATAAGTCTCTGGACAGT	480
D	b	665	ATCTCTGTGGGATTCATATGATCTCTTATCAGTGGCTCTCTCAATAAGTCTCTGGACAGT	724
Q	y	481	GGCTCTGAGCAGAAAGCGCAGTGTCAATCATATGCTTAGAGCTGAATCTCTATAAATGGCT	540
D	b	725	GGCTCTGAGCAGAAAGCGCAGTGTCAATCATATGCTTAGAGCTGAATCTCTATAAATGGCT	784
Q	y	541	AAGCTGACAGACCATGAATATATTTGCTTGGTGGTGGCTGCTGCTGCAATTTTTCACA	600
D	b	785	AAGCTGACAGACCATGAATATATTTGCTTGGTGGTGGCTGCTGCTGCAATTTTTCACA	844
Q	y	601	CTCAGCATCTGTATCTGTGATCATTTGGGCTTCTGTTAAAAGTGAAGGTCCCAATCG	660
D	b	845	CTCAGCATCTGTATCTGTGATCATTTGGGCTTCTGTTAAAAGTGAAGGTCCCAATCG	904
Q	y	661	GGGCTGGGGGTTTCTCAGAGGAAGGCACTGACCAATCATATGACCTGATCATCTTCT	720
D	b	905	GGGCTGGGGGTTTCTCAGAGGAAGGCACTGACCAATCATATGACCTGATCATCTTCT	964
Q	y	721	TTCTTGTGTTTCTGACCTTATCACAACCTGAGAACCTGTCATTCAGCATGAGAAAGTG	780
D	b	965	TTCTTGTGTTTCTGACCTTATCACAACCTGAGAACCTGTCATTCAGCATGAGAAAGTG	1022
Q	y	781	GGTTTATGCAAAAGACAGACTGATTAAGCTTGTGTTATCACACTGCTTGGCAGACGCG	840
D	b	1025	GGTTTATGCAAAAGACAGACTGATTAAGCTTGTGTTATCACACTGCTTGGCAGACGCG	1084
Q	y	841	AATGCTGCTTCAATCCTCTGCTCTATTACTTTGCTGGGAGAAATTTTAAAGACAGACTA	900
D	b	1085	AATGCTGCTTCAATCCTCTGCTCTATTACTTTGCTGGGAGAAATTTTAAAGACAGACTA	1144
Q	y	901	AAGCTGCACTCAGAAAAGGCACTCACAGAAAGGCAAAAGCAAAAGTGTGTTTCCCTGT	960
D	b	1145	AAGCTGCACTCAGAAAAGGCACTCACAGAAAGGCAAAAGCAAAAGTGTGTTTCCCTGT	1204
Q	y	961	AGTGTGTGTTGAGAAAGAAACAAAGATATA	993
D	b	1205	AGTGTGTGTTGAGAAAGAAACAAAGATATA	1237
RESULT 2				
US-09-044-404A-1				
Sequence 1, Application US/09044404A				
Patent No. 6200775				
GENERAL INFORMATION:				
APPLICANT: SATHE, GANESH				
APPLICANT: HALSEY, WENDY				
APPLICANT: ELLIS, CATHERINE				
APPLICANT: AMES, ROBERT				
APPLICANT: FOLEY, JAMES				
APPLICANT: SARAU, HENRY				
TITLE OF INVENTION: CDNA CLONE HMTMP81 THAT ENCODES				
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR				
NUMBER OF SEQUENCES: 2				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: SmithKline Beecham Corporation				
STREET: 790 Swedeland Road, P.O. Box 1539				
CITY: King of Prussia				
STATE: PA				
COUNTRY: USA				
ZIP: 19406				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Diskette				
COMPUTER: IBM Compatible				
OPERATING SYSTEM: DOS				

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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH-70001-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-03-044-404A-1

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Query Match	Similarity	14.6%	Score 145.2	DB 3	Length 1578
Best Local	Similarity	15.5%	Pred. 1.1e-35		
Matches	451	Conservative	0	Mismatches	398
				Indels	27
				Gaps	4
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Db	514	CACATATTGATGACTTCCGCAATCAAGATATTCACCTTGATCTATGATCTCTGTGT	573		
Qy	105	GGAGCTCTTGAGAAATAGGTTGTGCATATATATGTTTCTCGACGCTTATAGAAGTCCAC	164		
Db	574	AGGCTTTCTTTGGCAATGAGCTTTTGCTCTATGTCTCATATAAACCTATCCAGAAATC	633		
Qy	165	ATCTGTAAGCTTTTCACTAGCTAAATCTGGCCATTTCAGATCTCTGTTCATTAAGCAGCT	224		
Db	634	AGCCTTCCAGATATACATGATTAATTAATTAGCAGTACAGATCTTAATTGTGTGCACACT	693		
Qy	225	TTCCTTCAAGGCTGACATATATCTTAAGAGCTCCAAATTTGATTTGGAGACCTGGCCTG	284		
Db	694	GCCCTCCGCTGTCTATTAATGTCACAAAGCAATTTGGCTCTTGGTGACTTCTGTG	753		
Qy	285	CAGATATATGCTATATCTTCTGTATGTCAACATGTACAGCAGATATTTATTTCTGAACCT	344		
Db	754	CCGCTCAGAACCTATGCTTTGTATGTCAACCTCATATGTATGACATCTTATTAGAAGC	813		
Qy	345	GCTAAGTGTGTGGCTTTCCTGGGAATGTTCAACCCCTTTGGCTTGCATGTACCAAG	404		
Db	814	CATGAGCTTTTTCGGTGCAATGGAAATGTTTTTCCAGTCCAGAACATTAATTTGGTTAC	873		
Qy	405	CATCAGAGATGCTGGAATCTCTGTGGATCATATGATCCTT---ATCATGGCTTCTC	461		
Db	874	ACAGAAAAAACCAAGCTTTGTGTGTGTATGATTTGGATTTTGTGATTTTGAACAATTC	933		
Qy	462	AATATATCTCTGTGACATGTGCTGTGACGAACGCACTGTCAATCATATCTTAAAGCT	521		
Db	934	TCCATTTTCTATATGCCAAACCAAAAAGATGGAAAAATATATCCAAAGTCTTTGAGCC	993		
Qy	522	GAATCTTATTAATAATGCTAAGCTGCA-----GACCATGAACATATATGCTTGGTGT	575		
Db	994	CCCAAGACATATAAATTAATAATCATGTTTGTGTCTTGATTAATGTATGATTTGT	1055		
Qy	576	GGGCTGCTGCTGTCATTTTTCACATCAGCATCTGTATCTGTGATCATTTGGGTTCT	635		
Db	1054	TGGCTTATATATCCCTTTTGTATTAATATGTCTGTACACAAATGATCATTTTGACCTT	1113		
Qy	636	GTTTAAATGTAGAGTCCCAAAATCGGGGCTGCGGGTTTTCACAGAAAGCACTGACAC	695		
Db	1114	ACTTAAAAAATTCATATGAAAAAATCTGTCAAG-----TCATAAAAAGCTATAGGAT	1167		